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(54) Title: DETECTION OF FUNGAL PATHOGENS USING THE POLYMERASE CHAIN REACTION

(57) Abstract

DNA sequences from the Internal Transcribed Spacer of the ribosomal RNA gene region are described for different species and strains of *Septoria*, *Pseudocercosporella*, *Fusarium* and *Mycosphaerella*. Specific primers from within these sequences are identified as being useful for the identification of the fungal isolates using PCR-based techniques.

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Seq. 83 comprise 59

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DETECTION OF FUNGAL PATHOGENS USING THE POLYMERASE CHAIN REACTION

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FIELD OF THE INVENTION

The present invention relates to the use of species-specific primers in polymerase chain
10 reaction assays for the detection of fungal pathogens. The use of these primers enables the
detection of specific isolates of fungal pathogens and the monitoring of disease development
in plant populations.

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BACKGROUND OF THE INVENTION

Diseases in plants cause considerable crop loss from year to year resulting both in economic
deprivation to farmers and additionally in many parts of the world to shortfalls in the
nutritional provision for local populations. The widespread use of fungicides has provided
20 considerable security against plant pathogen attack. However, despite \$1 billion worth of
expenditure on fungicides, worldwide crop losses amounted to approximately 10% of crop
value in 1981 (James, 1981; *Seed Sci. & Technol.* 9: 679-685).

The severity of the destructive process of disease depends on the aggressiveness of the
25 pathogen and the response of the host. One aim of most plant breeding programs is to
increase the resistance of host plants to disease. Typically, different races of pathogens
interact with different varieties of the same crop species differentially, and many sources of
host resistance only protect against specific pathogen races. Furthermore, some pathogen
races show early signs of disease symptoms, but cause little damage to the crop. Jones and
30 Clifford (1983; *Cereal Diseases*, John Wiley) report that virulent forms of the pathogen are
expected to emerge in the pathogen population in response to the introduction of resistance
into host cultivars and that it is therefore necessary to monitor pathogen populations. In
addition, there are several documented cases of the evolution of fungal strains which are

resistant to particular fungicides. As early as 1981, Fletcher and Wolfe (1981; *Proc. 1981 Brit. Crop Prot. Conf.*) contended that 24% of the powdery mildew populations from spring barley, and 53% from winter barley showed considerable variation in response to the fungicide triadimenol and that the distribution of these populations varied between varieties 5 with the most susceptible variety also giving the highest incidence of less susceptible types. Similar variation in the sensitivity of fungi to fungicides has been documented for wheat mildew (also to triadimenol), *Botrytis* (to benomyl), *Pyrenophora* (to organomercury), *Pseudocercospora* (to MBC-type fungicides) and *Mycosphaerella fijiensis* to triazoles to mention just a few (Jones and Clifford; Cereal Diseases, John Wiley, 1983).

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Cereal species are grown world-wide and represent a major fraction of world food production. Although yield loss is caused by many pathogens, the necrotizing pathogens *Septoria* and *Pseudocercospora* are particularly important in the major cereal growing areas of Europe and North America (Jones and Clifford; Cereal Diseases, John Wiley, 1983).

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In particular, the differential symptomology caused by different isolates and species of these fungi make the accurate predictive determination of potential disease loss difficult. Consequently, the availability of improved diagnostic techniques for the rapid and accurate identification of specific pathogens will be of considerable use to field pathologists.

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Four *Septoria* species parasitize the small grain species. *Septoria tritici* is the causative agent of leaf blotch and is virulent on wheat but also parasitizes triticale and rye. It typically causes leaf necrosis. *Septoria nodorum* is the causative agent of glume blotch and is parasitic on wheat, triticale, rye and barley and although mainly restricted to glumes is also found on leaf blades and sheaths. *Septoria avenae* is parasitic on oats, wheat and triticale and *Septoria passerinii* is restricted to barley. *Septoria* diseases occur in all wheat growing areas at economically important levels. Different *Septoria* diseases frequently occur concurrently within fields and on individual plants, where the disease symptoms may be collectively referred to as the "Septoria complex". Typically, the most commonly found species are *S. tritici* and *S. nodorum*. According to Wiese (1977; Compendium of Wheat Diseases, Amer.

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Phytopath. Soc. pages 42-45), the Septoria complex presently destroys nearly 2% of the world's wheat annually, the yield loss being mainly the result of impaired grain filling. Fungicide treatments can save up to 20% in cases of severe *Septoria* infection, but it is often difficult to distinguish between the different *Septoria* species at the onset of infection and this

makes the decision whether or not to invest in fungicide use difficult because different cultivars display differing degrees of resistance to the various *Septoria* species.

The eyespot disease of cereals is caused by the fungus *Pseudocercosporella herpotrichoides* and is restricted to the basal culm of the plant. Wheat, rye, oats and other grasses are susceptible to the eyespot disease which occurs in cool, moist climates and is prevalent in Europe, North and South America, Africa and Australia. Wheat is the most susceptible cereal species, but isolates have been identified which are also virulent on other cereals. The R-strain of the fungus, for example, has also been isolated from rye and grows more slowly on wheat than the W-strain which has been isolated from wheat. Although eyespot may kill tillers or plants outright, it more usually causes lodging and/or results in a reduction in kernel size and number. Yield losses associated with eyespot are of even greater magnitude than those associated with *Septoria tritici* and *Septoria nodorum*. Typical control measures for eyespot include treatment with growth regulators to strengthen internodes, and fungicide treatment. However, the differing susceptibility of cultivars to different strains of the fungus render the predictive efficacy of fungicide treatments difficult.

Sigatoka leaf spot of banana occurs in two forms each of which is caused by a different fungus. The economically important Black Sigatoka is caused by *Mycosphaerella fijiensis*, whereas the less economically significant Yellow Sigatoka is caused by *Mycosphaerella musicola* (Johanson and Jeger, 1993; Mycol. Res. 97: 670-674). Black Sigatoka is the major problem in banana causing severe losses of 30% and more. Due to occurrence of fungicide resistance in *Mycosphaerella fijiensis*, usage of fungicide should best be limited to prevent the further occurrence of resistance. Consequently, the availability of diagnostic tools will provide an important means of identifying the appropriate circumstances in which to utilize fungicides without unnecessarily risking the development of further resistance.

Thus, there is a real need for the development of technology which will allow the identification of specific races of pathogen fungi early in the infection process. By identifying the specific race of a pathogen before disease symptoms become evident in the crop stand, the agriculturist can assess the likely effects of further development of the pathogen in the crop variety in which it has been identified and can choose an appropriate fungicide if such application is deemed necessary.

SUMMARY OF THE INVENTION

- 5 The present invention is drawn to methods of identification of different pathotypes of plant pathogenic fungi. The invention provides DNA sequences which show variability between different fungal pathotypes. Such DNA sequences are useful in the method of the invention as they can be used to derive primers for use in polymerase chain reaction (PCR)-based diagnostic assays. These primers generate unique fragments in PCR reactions in which the
- 10 DNA template is provided by specific fungal pathotypes and can thus be used to identify the presence or absence of specific pathotypes in host plant material before the onset of disease symptoms.

This invention provides the possibility of assessing potential damage in a specific crop variety-pathogen strain relationship and of utilizing judiciously the diverse armory of fungicides which is available. Furthermore, it can be used to provide detailed information on the development and spread of specific pathogen races over extended geographical areas. The invention provides a method of detection which is especially suitable for diseases with a long latent phase such as those caused by *Septoria nodorum* or *Septoria tritici* on wheat and

20 *Mycosphaerella fijiensis* on banana.

Kits useful in the practice of the invention are also provided. The kits find particular use in the identification of *Septoria*, *Pseudocercosporella*, *Fusarium*, and *Mycosphaerella* pathogens.

DESCRIPTION OF THE FIGURES

Figure 1 Alignment of Internal Transcribed Spacer Sequences from *Septoria tritici*,
Septoria nodorum, *Pseudocercosporella herpotrichoides* strain W (two variants),
Pseudocercosporella herpotrichoides strain R, *Mycosphaerella fijiensis*, and *Mycosphaerella*
30 *musicola*.

Figure 2 Alignment of the Internal Transcribed Spacer Sequences from *Septoria nodorum* and *Septoria avenae* f.sp. *triticea*.

Figure 3 Alignment of the Internal Transcribed Spacer Sequences from *Fusarium graminearum*, *Fusarium culmorum*, *Fusarium moniliforme* and *Microdochium nivale*.

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DETAILED DESCRIPTION OF THE INVENTION

The present invention provides unique DNA sequences which are useful in identifying different pathotypes of plant pathogenic fungi. Particularly the DNA sequences can be used
10 as primers in PCR based analysis for the identification of fungal pathotypes. The DNA sequences of the invention include the Internal Transcribed Spacer (ITS) of the ribosomal RNA gene regions of particular fungal pathogens as well as primers which are derived from these regions which are capable of identifying the particular pathogen. These ITS DNA sequences from different pathotypes within a pathogen species or genus which vary between
15 the different members of the species or genus can be used to identify those specific members.

Biomedical researchers have used PCR-based techniques for some time and with moderate success to detect pathogens in infected animal tissues. Only recently, however, has this technique been applied to detect plant pathogens. The presence of *Gaumannomyces graminis*
20 in infected wheat has been detected using PCR of sequences specific to the pathogen mitochondrial genome (Schlessner *et al.*, 1991; *Applied and Environ. Microbiol.* 57: 553-556) and random amplified polymorphic DNA (*i.e.* RAPD) markers were able to distinguish numerous races of *Gremmeniella abietina*, the causal agent of scleroderris canker in conifers.

25 Ribosomal genes are suitable for use as molecular probe targets because of their high copy number. Despite the high conservation between mature rRNA sequences, the non-transcribed and transcribed spacer sequences are usually poorly conserved and are thus suitable as target sequences for the detection of recent evolutionary divergence. Fungal rRNA genes are organized in units each of which encodes three mature subunits of 18S, 5.8S,
30 and 28S respectively. These subunits are separated by two internal transcribed spacers, ITS1 and ITS2, of around 300 bp (White *et al.*, 1990; In: PCR Protocols; Eds.: Innes *et al.*; pages 315-322). In addition, the transcriptional units are separated by non-transcribed spacer

sequences (NTSs). The ITS and NTS sequences are particularly suitable for the detection of specific pathotypes of different fungal pathogens.

The DNA sequences of the invention are from the Internal Transcribed Spacer (ITS) of the 5 ribosomal RNA gene region of different plant pathogens. The ITS DNA sequences from different pathotypes within a pathogen species or genus vary between the different members of the species or genus. Once having determined the ITS sequences of a pathogen, these sequences can be aligned with other ITS sequences. In this manner, primers can be derived from the ITS sequences. That is, primers can be designed based on regions within the ITS 10 regions that contain the greatest differences in sequence among the fungal pathotypes. These sequences and primers based on these sequences can be used to identify specific pathogen members.

Particular DNA sequences of interest include ITS DNA sequences from *Septoria*, 15 particularly, *Septoria nodorum* and *Septoria tritici*; *Mycosphaerella*, particularly *Mycosphaerella fijiensis* and *Mycosphaerella musicola*; *Pseudocercophorella*, particularly *Pseudocercosporella herpotrichoides*, more particularly for the W-strain and the R-strain of *Pseudocercosporella herpotrichoides*, *Fusarium*, particularly *F. graminearum*, *F. culmorum*, *F. moniliforme* and *Microdochium nivale*. Such ITS DNA sequences as well as primers of 20 interest are given in SEQ ID NO: 1 - 47 and SEQ ID NO.: 50-86. The sequences find use in the PCR-based identification of the pathotypes of interest.

Methods for the use of the primer sequences of the invention in PCR analysis are well known in the art. For example, see US Patent Nos. 4,683,195 and 4,683,202 as well as Schlesser *et* 25 *al.* (1991) *Applied and Environ. Microbiol.* 57:553-556. See also, Nazar *et al.* (1991); *Physiol. and Molec. Plant Pathol.* 39: 1-11) which used PCR amplification to exploit differences in the ITS regions of *Verticillium albo-atrum* and *Verticillium dahliae* and therefore distinguish between the two species; and Johanson and Jeger (1993; *Mycol. Res.* 97: 670-674) who used similar techniques to distinguish the banana pathogens *Mycosphaerella fijiensis* and *Mycosphaerella musicola*.

The ITS DNA sequences of the invention can be cloned from fungal pathogens by methods known in the art. In general, the methods for the isolation of DNA from fungal isolates are

known. See, Raeder & Broda (1985) *Letters in Applied Microbiology* 2:17-20; Lee *et al.* (1990) *Fungal Genetics Newsletter* 35:23-24; and Lee and Taylor (1990) In: *PCR Protocols: A Guide to Methods and Applications*, Innes *et al.* (Eds.); pages 282-287.

5 Alternatively, the ITS regions of interest can be determined by PCR amplification. Primers to amplify the entire ITS region were designed according to White *et al.* (1990; In: *PCR Protocols*; Eds.: Innes *et al.* pages 315-322) and the amplified ITS sequence was subcloned into the pCRII cloning vector. The subcloned sequence included the lefthand ITS (ITS1), the righthand ITS (ITS2) as well as the centrally located 5.8S rRNA gene. This was undertaken
10 for *Septoria nodorum* and *Septoria tritici*, numerous *Pseudocercospora* isolates and *Mycosphaerella fijiensis*, *Mycosphaerella musicola*, *Septoria avenae triticea*, *F. graminearum*, *F. culmorum*, *F. moniliforme* and *Microdochium nivale*.

15 The ITS sequences were determined and within each pathogen group the sequences were compared to locate divergences which might be useful to test in PCR to distinguish the different species and/or strains. The sequences of the ITS regions which were determined are shown as Sequence ID's 1 to 6, 47, and 82-86 and also in Figures 1, 2 and 3. From the identification of divergences numerous primers were synthesized and tested in PCR-amplification. Templates used for PCR-amplification testing were firstly purified pathogen
20 DNA, and subsequently DNA isolated from infected host plant tissue. Thus it was possible to identify pairs of primers which were diagnostic *i.e.* which identified one particular pathogen species or strain but not another species or strain of the same pathogen. Preferred primer combinations are able to distinguish between the different species or strains in infected host tissue *i.e.* host tissue which has previously been infected with a specific
25 pathogen species or strain.

This invention provides numerous primer combinations which fulfill this criterion for different *Septoria*, *Mycosphaerella*, and *Fusarium* species and different strains of *Pseudocercospora*. The primers of the invention are designed based on sequence differences among the fungal ITS regions. A minimum of one base pair difference between sequences can permit design of a discriminatory primer. Primers designed to a specific fungal DNA's ITS region can be used in combination with a primer made to a conserved sequence region within the ribosomal DNA's coding region to amplify species-specific PCR
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fragments. In general, primers should have a theoretical melting temperature between about 60 to about 70 degree C to achieve good sensitivity and should be void of significant secondary structure and 3' overlaps between primer combinations. Primers are generally at least about 5 to about 10 nucleotide bases.

5

The usefulness of cloned ITS sequences for the selection of primers for diagnostic purposes is largely due to their rapid evolutionary divergence. For example, W-type and R-type isolates of the pathogen *Pseudocercospora herpotrichoides* were found to have divergent ITS sequences from which diagnostic primers were developed. However, the rapid 10 divergence within the ITS sequence is apparent from the observation that two different sequence variants of the W-type were identified. The sequence identity within the W-type was 99.4 %, whereas that between W and R-types was 98.6 % suggesting a closer evolutionary relationship between the two W variants than was found between the W and the R-types. This closer relationship is also apparent from their similar host pathogenicity of the 15 two isolates with divergent ITS sequences.

In addition to developing primers from ITS-derived sequences for PCR diagnosis of fungal isolates, the invention also encompasses the identification of primers from RAPD primer libraries which can distinguish between *Septoria nodorum* and *Septoria tritici* when used in 20 PCR. The primers screened are commercially available and were obtained from Operon Technologies Incorporated (Alameda, CA). Screening on *Septoria* genomic DNA identified two primers which were able to detect only *S. tritici* and three which were able to detect only *S. nodorum*.

25 The present invention lends itself readily to the preparation of "kits" containing the elements necessary to carry out the process. Such a kit may comprise a carrier being compartmentalized to receive in close confinement therein one or more container means, such as tubes or vials. One of said container means may contain unlabeled or detectably labeled DNA primers. The labeled DNA primers may be present in lyophilized form, or in 30 an appropriate buffer as necessary. One or more container means may contain one or more enzymes or reagents to be utilized in PCR reactions. These enzymes may be present by themselves or in admixtures, in lyophilized form or in appropriate buffers.

Finally, the kit may contain all of the additional elements necessary to carry out the technique of the invention, such as buffers, extraction reagents, enzymes, pipettes, plates, nucleic acids, nucleoside triphosphates, filter paper, gel materials, transfer materials, autoradiography supplies, and the like.

5

The examples below show, without limitation, typical experimental protocols which can be used in the isolation of ITS sequences, the selection of suitable primer sequences, the testing of primers for selective and diagnostic efficacy, and the use of such primers for disease and fungal isolate detection. Such examples are provided by way of illustration and not by way 10 of limitation.

EXAMPLES

15 **Example 1: Fungal isolates and genomic DNA extraction**

Viable fungal isolates of *S. nodorum*, *S. tritici*, *S. passerini*, *S. glycines*, *Pseudocercosporella herpotrichoides*, *Pseudocercosporella aestiva*, *Mycosphaerella citri*, *Mycosphaerella graminicola*, *Mycosphaerella fijiensis* and *Mycosphaerella musicola* were obtained from the American Type Culture Collection. *Fusarium culmorum* and *Fusarium graminearum* isolates were obtained from Dr. Paul Nelson from Penn State University. An isolate of *Michrodochium nivale* (syn. *Fusarium nivale*) was received from Ciba- Basel and an isolate of *Fusarium moniliforme* was received from Dr. Loral Castor. Fungi were grown in 150 ml potato dextrose broth inoculated with mycelial fragments from PDA (Potato Dextrose Agar) cultures. Cultures were incubated on an orbital shaker at 28°C for 7-11 days. Mycelia were 25 pelleted by centrifugation and then ground in liquid nitrogen and total genomic DNA extracted using the protocol of Lee and Taylor (1990; In: *PCR Protocols: A Guide to Methods and Applications*; Eds.: Innes *et al.*; pages 282-287).

Dr. Bruce McDonald from Texas A&M University supplied genomic DNA from ten isolates 30 of *S. nodorum* and nine isolates of *S. tritici*. Dr. Chris Caten of Birmingham University provided six isolates of *Septoria nodorum* purified fungal DNA. Purified genomic DNA from 12 isolates of *Pseudocercosporella herpotrichoides* was obtained from Dr. Paul Nicholson of the John Innes Centre, Norwich, UK. Six of these isolates are of the W-type;

the other six isolates are of the R-type. These isolates were typed based on pathogenicity and RFLP studies. Andrea Johanson of the Natural Resources Institute supplied genomic DNA of six isolates of *M. musicola*, six isolates of *M. fijiensis* and a single isolate of *Mycosphaerella musae*. Purified genomic DNA from *Septoria avenae* f. sp. *triticea* 5 ATCC#26380 was supplied by Dr. Peter Ueng from the USDA at Beltsville, Maryland.

Table 1: Source of Test Isolates

<u>Isolate</u>	<u>Species</u>	<u>Origin</u>	<u>Source</u>
ATCC#24425	<i>S. nodorum</i>	Montana	ATCC ¹
XA1.1	<i>S. nodorum</i>	Texas	B. McDonald ²
Xa5A.2	<i>S. nodorum</i>	Texas	B. McDonald
YA3.1	<i>S. nodorum</i>	Texas	B. McDonald
XD2.1	<i>S. nodorum</i>	Texas	B. McDonald
YB2.2	<i>S. nodorum</i>	Texas	B. McDonald
93HBh6a	<i>S. nodorum</i>	Oregon	B. McDonald
93A3a	<i>S. nodorum</i>	Oregon	B. McDonald
93AYa	<i>S. nodorum</i>	Oregon	B. McDonald
93HBh8a	<i>S. nodorum</i>	Oregon	B. McDonald
93C5a	<i>S. nodorum</i>	Oregon	B. McDonald
ATCC#26517	<i>S. tritici</i>	Minnesota	ATCC
BS3	<i>S. nodorum</i>	Ireland	C. Caten ³
BS6	<i>S. nodorum</i>	Ireland	C. Caten
BS175	<i>S. nodorum</i>	England	C. Caten
BS425	<i>S. nodorum</i>	England	C. Caten
alpha'5	<i>S. nodorum</i>	France	C. Caten
m300	<i>S. nodorum</i>	England	C. Caten
TKV2a	<i>S. tritici</i>	Turkey	B. McDonald
SYK2	<i>S. tritici</i>	Syria	B. McDonald
ISZC36.2	<i>S. tritici</i>	Israel	B. McDonald
CNRC4a.1	<i>S. tritici</i>	Canada	B. McDonald
ALA1a	<i>S. tritici</i>	Algeria	B. McDonald
ETK1	<i>S. tritici</i>	Ethiopia	B. McDonald
GEB2a.1	<i>S. tritici</i>	Germany	B. McDonald
UK92D2	<i>S. tritici</i>	United Kingdom	B. McDonald
DNB1a	<i>S. tritici</i>	Denmark	B. McDonald
ATCC#38699	<i>S. glycines</i>	Illinois	ATCC
ATCC#22585	<i>S. passerini</i>	Minnesota	ATCC
ATCC#42040	<i>P. herpotrichoides</i> -wheat		ATCC
ATCC#62012	<i>P. aestiva</i>	Germany	ATCC
ATCC#60972	<i>P. herp. var. herp.- barley</i>	Germany	ATCC
W1	<i>P. herpotrichoides</i>	United Kingdom	P. Nicholson ⁴
W2	<i>P. herpotrichoides</i>	United Kingdom	P. Nicholson
W3	<i>P. herpotrichoides</i>	United Kingdom	P. Nicholson
W4	<i>P. herpotrichoides</i>	United Kingdom	P. Nicholson

W5	<i>P. herpotrichoides</i>	New Zealand	P. Nicholson
W6	<i>P. herpotrichoides</i>	Italy	P. Nicholson
R1	<i>P. herpotrichoides</i>	Belgium	P. Nicholson
R2	<i>P. herpotrichoides</i>	New Zealand	P. Nicholson
R3	<i>P. herpotrichoides</i>	Germany	P. Nicholson
R4	<i>P. herpotrichoides</i>	Sweden	P. Nicholson
R5	<i>P. herpotrichoides</i>	United Kingdom	P. Nicholson
R6	<i>P. herpotrichoides</i>	United Kingdom	P. Nicholson
ATCC#22116	<i>M. fijiensis</i>	Philippines	ATCC
ATCC#22115	<i>M. musicola</i>	Philippines	ATCC
ATCC#24046	<i>M. citri</i>	Florida	ATCC
ATCC#62714	<i>M. graminicola</i>	Montana	ATCC
PA92	<i>M. fijiensis</i>	Panama	A. Johanson ⁵
PNG291	<i>M. fijiensis</i>	Papua New Guinea	A. Johanson
GH6-3	<i>M. fijiensis</i>	Ghana	A. Johanson
TG120	<i>M. fijiensis</i>	Tonga	A. Johanson
HSB4	<i>M. fijiensis</i>	Honduras	A. Johanson
RT689	<i>M. fijiensis</i>	Rarotonga (Cook Is.)	A. Johanson
CR548	<i>M. musicola</i>	Costa Rica	A. Johanson
CM61	<i>M. musicola</i>	Cameroon	A. Johanson
CU823	<i>M. musicola</i>	Cuba	A. Johanson
MQ103	<i>M. musicola</i>	Martinique	A. Johanson
CI31	<i>M. musicola</i>	Ivory Coast	A. Johanson
CB90	<i>M. musicola</i>	Colombia	A. Johanson
BD1-4	<i>M. musae</i>	Barbados	A. Johanson
ATCC#44234	<i>Ceratobasidium cereale</i>	Netherlands	ATCC
ATCC#11404	<i>Drechslera sorokiniana</i>	Minnesota	ATCC
R-5126	<i>F. culmorum</i>	Minnesota	P. Nelson ⁶
R-5106	<i>F. culmorum</i>	Michigan	P. Nelson
R-5146	<i>F. culmorum</i>	Finland	P. Nelson
R-8417	<i>F. graminearum</i>	Italy	P. Nelson
R-8422	<i>F. graminearum</i>	Canada	P. Nelson
R-8546	<i>F. graminearum</i>	Bulgaria	P. Nelson
4551	<i>F. moniliforme</i>	Indiana	L. Castor ⁷
92	<i>M. nivale</i>	-----	Ciba Basel ⁸
ATCC#26380	<i>S. avenae</i> f.sp. <i>triticea</i>	Minnesota	P. Ueng ⁹

1 American Type Culture Collection, Rockville, Maryland USA

2 Dr. Bruce McDonald, Texas A&M University, USA

3 Dr. Chris Caten, Birmingham University, UK

4 Dr. Paul Nicholson, John Innes Centre, UK

5 Dr. Andrea Johanson, Natural Resources Institute, UK

6 Dr. Paul Nelson, Penn State University

7 Dr. Loral Castor, Ciba Seeds Research, Bloomington, Illinois

8 Ciba-Geigy Limited, Basel, Switzerland

9 Dr. Peter Ueng, USDA, Beltsville, Maryland

Example 2: Isolation of the internal transcribed spacer (ITS) regions

The approximately 550 bp internal transcribed spacer region fragments were PCR amplified from 25 ng of genomic DNA isolated from *S. nodorum* (ATCC#24425), *S. tritici* (ATCC#26517), *Pseudocercosporella herpotrichoides* isolates R1, R2, W2 and W5, *M.*

- 5 *fijiensis* (ATCC#22115) and *M. musicola* (ATCC#22115) using 50 pmol of primers ITS1 (5'-TCCGTAGGTGAAACCTGCGG-3'; SEQ ID NO: 38) and ITS4 (5'-TCCTCCGCTTATTGATATGC-3'; SEQ ID NO:41). PCRs were performed as described in EXAMPLE 4 except that reactions were done in 100 µl and annealing was done at of 50°C. The ITS fragments were purified by isopropanol precipitation according to Maniatis et al.
- 10 (1982; *Molecular Cloning*; Eds.: Maniatis et al.; pages 461-462). The DNA was resuspended in 50 µl dH₂O and cloned using the Invitrogen Corporation's (San Diego, CA) TA Cloning Kit (part no. K2000-01) using the pCRII cloning vector. The DNA sequences of the ITS regions were determined by the dideoxy method using the Applied Biosystems (Foster City, CA) automated sequencer model 373A with the primers ITS1 (see sequence above), ITS2
- 15 (5'-GCTGCGTTCTCATCGATGC-3'; SEQ ID NO:39), ITS4 (see sequence above) and the M13 universal -20 (5'-GTAAAACGACGGCCAGT-3'; SEQ ID NO:48) and Reverse (5'-AACAGCTATGACCATG-3'; SEQ ID NO:49) primers. The ITS primers ITS1 (SEQ ID NO:38), ITS2 (SEQ ID NO:39), ITS3 (SEQ ID NO:40), and ITS4 (SEQ ID NO:41) used for cloning the ITS regions are detailed in White et al. (1990; In: *PCR Protocols*; Eds.: Innes et
- 20 al. pages 315-322).

In addition, the internal transcribed spacer regions were PCR amplified from 25 ng of genomic DNA from *S. avenae* f.sp. *triticea*, *M. nivale*, *F. moniliforme* (#4551), *F. graminearum* isolates R-8417, R-8546 and R-8422 and *F. culmorum* isolates R-5126, R-25 5106 and R-5146. PCR products were purified using Promega's Wizard DNA Clean-up kit (Madison, WI). The DNA sequences of the ITS regions were determined as described above using the ITS1 (SEQ ID NO:38), ITS2 (SEQ ID NO:39), ITS3 (SEQ ID NO:40) and ITS4 (SEQ ID NO:41) primers. Sequencing reactions were combined with the three isolates of *F. culmorum* and *F. graminearum* to generate a consensus sequence for *F. culmorum* and *F. 30 graminearum*.

Example 3: DNA extraction from wheat and banana leaves

DNA was extracted from wheat leaves using a modified version of the Rapid DNA Extraction protocol from the MicroProbe Corporation's (Garden Grove, CA) IsoQuick Nucleic Acid Extraction Kit (cat# MXT-020-100). Typical yields were 5-10 µg of total DNA from 0.2 g of leaf tissue. Approximately 100 ng of total DNA were used in each PCR assay.

Modified Rapid DNA Extraction:

Before using kit for the first time, the entire contents of Reagent 2A (20 x Dye Concentrate) were added to Reagent 2 (Extraction Matrix).

(1) Approximately 0.2 g of leaf sample were added to a 1.5 ml eppendorf tube containing 50 µl sample buffer A and 50 µl #1 lysis solution. The leaf sample was ground with a Kontes pestle.

(2) Reagent 2 (Extraction Matrix) was shaken vigorously. 350 µl of reagent 2 were added to the sample lysate.

(3) 200 µl of Reagent 3 were added (Extraction Buffer) to the sample. The sample was vortexed 20 sec.

(4) Microcentrifugation at 12,000 x g for 5 min.

(5) The aqueous phase (upper layer) was transferred to a new microcentrifuge tube. This volume was typically about 200 µl.

(6) 0.1 x the volume of the aqueous phase of Reagent 4 (Sodium Acetate) to the aqueous phase sample.

(7) An equal volume of isopropanol was added to the aqueous phase sample followed by vortexing.

(8) Microcentrifugation at 12,000 x g for 10 min.

(9) The supernatant was discarded without disturbing the nucleic acid pellet. 0.5 ml of -20°C 70% ethanol was added to the pellet. The tube was vortexed to mix.

(10) Microcentrifugation at 12,000 x g for 5 min.

(11) The supernatant was discarded and the pellet was allowed to dry.

(12) The nucleic acid pellet was dissolved in 50 µl Reagent 5 (RNase-free water).

Example 4: Polymerase chain reaction amplification

Polymerase chain reactions were performed with the GeneAmp Kit from Perkin-Elmer/Cetus (Norwalk, CT; part no. N808-0009) using 50 mM KCl, 2.5 mM MgCl₂, 10 mM Tris-HCl, pH8.3, containing 100 μM of each TTP, dATP, dCTP, and dGTP, 50 pM primer, 2.5 units of

Taq polymerase and 25 ng of genomic DNA in a final volume of 50 μl. Reactions were run for 30 cycles of 15 s at 94°C, 15 s at 50°C, 60°C or 70°C, and 45 s at 72°C in a Perkin-Elmer/Cetus Model 9600 thermal cycler. The products were analyzed by loading 20 μl of each PCR sample on a 1.1-1.2% agarose gel and electrophoresed.

10 Example 5: Synthesis and Purification of Oligonucleotides

Oligonucleotides (primers) were synthesized on an Applied Biosystems 380A DNA synthesizer using B-cyanoethyl-phosphoramidite chemistry.

15 Example 6: Selection of species-specific primers

The ITS sequences of *S. nodorum*, *S. tritici*, *P. herpotrichoides* strains R and W, *M. fijiensis* and *M. musicola* were aligned (Fig. 1). The ITS sequences of *S. nodorum* and *S. avenae*. *triticea* were aligned (Fig. 2). An alignment was also made of the ITS sequences from *F. graminearum*, *F. culmorum*, *F. moniliforme* and *M. nivale* (Fig. 3). Sets of primers were

20 synthesized according to EXAMPLE 5 based on analysis of the aligned sequences. Primers were designed to regions containing the greatest differences in sequence among the fungal species for Figs. 1-2. In Fig 3, primers were designed to regions of highest homology within the ITS for *Fusarium*. In addition, the published ribosomal gene-specific primers ITS1 (SEQ ID NO:38), ITS2 (SEQ ID NO:39), ITS3 (SEQ ID NO:40) and ITS4 (SEQ ID NO:41) (White *et al.*, 1990; In: PCR Protocols; Eds.: Innes *et al.* pages 315-322) were synthesized
25 for testing in combination with the primers specific for the ITS region.

Table 2: Primer Design for Fungal Detection

30

<u>Primer Template</u>	<u>Primer Name</u>	<u>Primer Sequence</u>
<i>S. nodorum</i>	JB433	5' ACACCTCAGTAGTTACTACT 3' (SEQ ID NO:7)
<i>S. nodorum</i>	JB434	5' TGTGCTGCGCTTCAATA 3' (SEQ ID NO:8)
<i>S. nodorum</i>	JB525	5' GCGACTTGTGCTGCGCTTCAATA 3' (SEQ ID NO:9)

<i>S. nodorum</i>	JB527	5' CATTACACTCAGTAGTTACTACT 3' (SEQ ID NO:10)
<i>S. tritici</i>	JB445	5' CTGCGTCGGAGTTACG 3' (SEQ ID NO:11)
<i>S. tritici</i>	JB446	5' CGAGGCTGGAGTGGTGT 3' (SEQ ID NO:12)
<i>S. tritici</i>	JB526	5' CCCAGCGAGGCTGGAGTGGTGT 3' (SEQ ID NO:13)
<i>P. herp.</i>	JB536	5' CTGGGGGCTACCCTACTTGGTAG 3' (SEQ ID NO:14)
<i>P. herp.</i>	JB537	5' GGGGGCTACCCCTACTTGGTAG 3' (SEQ ID NO:15)
<i>P. herp.</i>	JB538	5' ACTTGGTAGGGTTAGAGTCGTCA 3' (SEQ ID NO:16)
<i>P. herp.</i>	JB539	5' CTTCGGTAAAGTTAGAGTCGTG 3' (SEQ ID NO:17)
<i>P. herp.</i>	JB540	5' GGGGCCACCCTACTTCGGTAA 3' (SEQ ID NO:18)
<i>P. herp.</i>	JB541	5' CCACTGATTTAGAGGCCGCGAG 3' (SEQ ID NO:19)
<i>P. herp.</i>	JB542	5' CCACTGATTTAGAGGCCGCGAA 3' (SEQ ID NO:20)
<i>P. herp.</i>	JB543	5' CCTGTAAAAAATTGGGGGTTA 3' (SEQ ID NO:21)
<i>P. herp.</i>	JB544	5' CCTGTAAAAAATTGGGGGTTG 3' (SEQ ID NO:22)
<i>M. fijiensis</i>	JB547	5' ATTACCGAGTGAGGGCTCACGC 3' (SEQ ID NO:23)
<i>M. fijiensis</i>	JB548	5' GTTGCTTCGGGGCGACCTGCG 3' (SEQ ID NO:24)
<i>M. fijiensis</i>	JB442	5' TCGGGGGCGACCTGCCG 3' (SEQ ID NO:25)
<i>M. fijiensis</i>	JB443	5' CCGGAGGCCGTCA 3' (SEQ ID NO:26)
<i>M. fijiensis</i>	JB545	5' CCACAAACGCTTAGAGACGGACAG 3' (SEQ ID NO:27)
<i>M. fijiensis</i>	JB546	5' CACCCGCACTCCGAAGCGAATT 3' (SEQ ID NO:28)
<i>M. fijiensis</i>	JB549	5' GATCCGAGGTCAACCTTGAATAA 3' (SEQ ID NO:29)
<i>M. fijiensis</i>	JB444	5' GGTCAACCTTGAATAA 3' (SEQ ID NO:30)
<i>M. musicola</i>	JB451	5' CCTTGTGAACCACACCT 3' (SEQ ID NO:31)
<i>M. musicola</i>	JB440	5' CTGCCGGCGAACCT 3' (SEQ ID NO:32)
<i>M. musicola</i>	JB449	5' ACCCTGCCGGCGAACCT 3' (SEQ ID NO:33)
<i>M. musicola</i>	JB448	5' GCGACCCCTGCCGGCGAAC 3' (SEQ ID NO:34)
<i>M. musicola</i>	JB441	5' TAGCCGGAGACTTGG 3' (SEQ ID NO:35)
<i>M. musicola</i>	JB450	5' TCTCGTCCGGAGTTCC 3' (SEQ ID NO:36)
<i>M. musicola</i>	JB452	5' CCGCGCTCCGGAGCGAAC 3' (SEQ ID NO:37)
18S rDNA	ITS1	5' TCCGTAGGTGAACCTGCGG 3' (SEQ ID NO:38)
5.8S rDNA	ITS2	5' GCTGCGTCTTCATCGATGC 3' (SEQ ID NO:39)
5.8S rDNA	ITS3	5' GCATCGATGAAGAACCGCAGC 3' (SEQ ID NO:40)
25S rDNA	ITS4	5' TCCTCCGCTTATTGATATGC 3' (SEQ ID NO:41)
<i>S. nodorum</i>	JB563	5' CTTGCCTGCCGGTTGGACAAATT 3' (SEQ ID NO:50)
<i>S. nodorum</i>	JB564	5' CTCAGTAGTTACTACTGTAAAAGG 3' (SEQ ID NO:51)
<i>S. nodorum</i>	JB565	5' CTTCTGGACGCAAGTGTGTTAC 3' (SEQ ID NO:52)
<i>Fusarium</i> spp.	JB566	✓5' GTTTTAGTGGAACTTCTGAGT 3' (SEQ ID NO:53)
<i>Fusarium</i> spp.	JB567	✓5' CGCAGGAACCCTAAACTCT 3' (SEQ ID NO:54)
<i>Fusarium</i> spp.	JB568	5' GCCCCGCCGAGG 3' (SEQ ID NO:55)
<i>Fusarium</i> spp.	JB569	✓5' RTWWTTWRTGGAMYYTCTGAGT 3' (SEQ ID NO:56)
<i>Fusarium</i> spp.	JB570	✓5' TATGTTGCCTCGGCGG 3' (SEQ ID NO:57)
<i>Fusarium</i> spp.	JB571	✓5' TAACGATATGTAAATTACTACGCT 3' (SEQ ID NO:58)
<i>Fusarium</i> spp. 19.	JB572	✗5' AAGTTGGGTTAACGGC 3' (SEQ ID NO:59)
<i>Fusarium</i> spp.	JB573	✓5' AGCGAGCCC GCCAC 3' (SEQ ID NO:60)
<i>Fusarium</i> spp.	JB574	✓5' CCATTGTGAACGTTACCTATAC 3' (SEQ ID NO:61)
<i>Fusarium</i> spp.	JB575	✓5' CGACCAGAGCGAGATGTA 3' (SEQ ID NO:62)
<i>Fusarium</i> spp.	JB576	✓5' GTGAACATACCTTATGTTGCC 3' (SEQ ID NO:63)
<i>Fusarium</i> spp.	JB577	✓5' GTTGCCCTCGGCGGATC 3' (SEQ ID NO:64)
<i>Fusarium</i> spp.	JB578	✓5' CCGCGACGATTACCAAG 3' (SEQ ID NO:65)

NOTE: *Fusarium* spp. includes *F. graminearum*, *F. culmorum*, *F. moniliforme* and *Michrodochium nivale* (syn. *F. nivale*).

5

Example 7: Selection of Random Amplified Polymorphic DNA (RAPD) primers

Two RAPD primer libraries (kits B and E) of twenty oligonucleotides each were purchased from Operon Technologies Incorporated (Alameda, CA). The primers were tested for their ability to differentiate purified genomic DNA of *S. nodorum*, *S. tritici*, *M. fijiensis* and *M. musicola*. The PCR conditions were essentially the same as described in EXAMPLE 4 except the number of PCR cycles was increased to 35, the annealing temperature was 30°C and only 5 picamoles of each primer were used. Five RAPD primers were identified that differentiate purified genomic DNA of *S. nodorum*, *S. tritici*, *M. fijiensis* and *M. musicola*.

15 Primers OPB-12 and OPE-6 produced a single fragment when amplified with *S. tritici* genomic DNA. Primers OPE-12, OPB-19 and OPE-15 produced single fragments from *S. nodorum* genomic DNA. Primers OPB-12 and OPE-6 did not produce any amplification products from *S. nodorum* *M. fijiensis* and *M. musicola* genomic DNA. Primers OPE-12, OPB-19 and OPE-15 did not amplify any fragments from genomic *S. tritici*, *M. fijiensis* or

20 *M. musicola* DNA.

Table 3: RAPD Primers for Septoria Diagnosis

25	<u>Source of template DNA</u>	<u>Primer</u>	<u>Sequence of primer</u>	<u>Approximate size of amplified fragment</u>
30	<i>S. tritici</i>	OPB-12	5'-CCTTGACGCA-3' (SEQ ID NO: 42)	1.3 kb
	<i>S. tritici</i>	OPE-6	5'-AAGACCCCTC-3' (SEQ ID NO: 43)	1.0 kb
	<i>S. nodorum</i>	OPE-12	5'-TTATCGCCCC-3' (SEQ ID NO: 44)	2.2 kb
	<i>S. nodorum</i>	OPB-19	5'-ACCCCCGAAG-3' (SEQ ID NO: 45)	1.1 kb
	<i>S. nodorum</i>	OPE-15	5'-ACGCACAACC-3' (SEQ ID NO: 46)	1.3 kb

35

Example 8: Determination of primer specificity to purified fungal genomic DNA

PCRs were performed according to EXAMPLE 4 using different primer combinations in an attempt to amplify a single species-specific fragment. Species-specific PCR amplification products were produced from primers designed from the ITS region between the 18S and 25S ribosomal DNA subunits of each fungal strain of interest.

Table 4: ITS-derived diagnostic PCR primers

<u>Source of template DNA</u>	<u>5'Primer</u>	<u>3'Primer</u>	<u>Approximate size of amplified fragment</u>
<i>Septoria nodorum</i>	JB433 (SEQ ID NO:7)	JB434 (SEQ ID NO:8)	448bp
	JB433 (SEQ ID NO:7)	ITS4 (SEQ ID NO:41)(JB415)	553bp
	ITS1 (SEQ ID NO:38)(JB410)	JB434 (SEQ ID NO:8)	478bp
	ITS3 (SEQ ID NO:40)(JB414)	JB434 (SEQ ID NO:8)	232bp*
	JB527 (SEQ ID NO:10)	JB525 (SEQ ID NO:9)	458bp
	JB564 (SEQ ID NO:51)	JB565 (SEQ ID NO:52)	480bp
	JB563 (SEQ ID NO:50)	JB565 (SEQ ID NO:52)	368bp
<i>Septoria tritici</i>	JB445 (SEQ ID NO:11)	ITS4 (SEQ ID NO:41)(JB415)	407bp
	ITS1 (SEQ ID NO:38)(JB410)	JB446 (SEQ ID NO:12)	345bp
	ITS3 (SEQ ID NO:40)(JB414)	JB446 (SEQ ID NO:12)	143bp*
	JB445 (SEQ ID NO:11)	JB446 (SEQ ID NO:12)	204bp
	*		
<i>M. fijiensis</i>	JB443 (SEQ ID NO:26)	ITS4 (SEQ ID NO:41)(JB415)	418bp
	ITS1 (SEQ ID NO:38)(JB410)	JB444 (SEQ ID NO:30)	482bp
	JB443 (SEQ ID NO:26)	JB444 (SEQ ID NO:30)	366bp*
	ITS3 (SEQ ID NO:40)(JB414)	JB444 (SEQ ID NO:30)	281bp*
	ITS1 (SEQ ID NO:38)(JB410)	JB549 (SEQ ID NO:29)	489bp
	*		
<i>M. musicola</i>	JB449 (SEQ ID NO:33)	ITS4 (SEQ ID NO:41)(JB415)	430bp
	JB448 (SEQ ID NO:34)	ITS4 (SEQ ID NO:41)(JB415)	449bp*
	JB448 (SEQ ID NO:34)	ITS2 (SEQ ID NO:39)(JB411)	138bp*
	JB450 (SEQ ID NO:36)	ITS4 (SEQ ID NO:41)(JB415)	390bp*
	*		

P. herpotrichoides

JB536 (SEQ ID NO:14)	JB541 (SEQ ID NO:19)	415bp [*]
JB536 (SEQ ID NO:14)	JB543 (SEQ ID NO:21)	502bp [*]
JB537 (SEQ ID NO:15)	JB541 (SEQ ID NO:19)	413bp [*]
JB537 (SEQ ID NO:15)	JB543 (SEQ ID NO:21)	500bp [*]
JB538 (SEQ ID NO:16)	JB541 (SEQ ID NO:19)	401bp [*]
JB538 (SEQ ID NO:16)	JB543 (SEQ ID NO:21)	488bp [*]
JB536 (SEQ ID NO:14)	ITS4 (SEQ ID NO:41)(JB415)	560bp [*]
JB537 (SEQ ID NO:15)	ITS4 (SEQ ID NO:41)(JB415)	558bp [*]
JB538 (SEQ ID NO:16)	ITS4 (SEQ ID NO:41)(JB415)	546bp [*]
ITS1 (SEQ ID NO:38)(JB410)	JB541 (SEQ ID NO:19)	482bp [*]
ITS1 (SEQ ID NO:38)(JB410)	JB543 (SEQ ID NO:21)	569bp [*]
ITS1 (SEQ ID NO:38)(JB410)	JB542 (SEQ ID NO:20)	482bp [*]
ITS1 (SEQ ID NO:38)(JB410)	JB544 (SEQ ID NO:22)	569bp ^{**}
JB540 (SEQ ID NO:18)	ITS4 (SEQ ID NO:41)(JB415)	558bp ^{**}
JB539 (SEQ ID NO:17)	ITS4 (SEQ ID NO:41)(JB415)	545bp ^{**}
JB540 (SEQ ID NO:18)	JB542 (SEQ ID NO:20)	413bp ^{**}
JB540 (SEQ ID NO:18)	JB544 (SEQ ID NO:22)	500bp ^{**}
JB539 (SEQ ID NO:17)	JB542 (SEQ ID NO:20)	400bp ^{**}
JB539 (SEQ ID NO:17)	JB544 (SEQ ID NO:22)	487bp ^{**}

Fusarium spp.

JB566 (SEQ ID NO:53)	ITS4 (SEQ ID NO:41)(JB415)	430bp ¹
JB566 (SEQ ID NO:53)	JB572 (SEQ ID NO:59)	346bp ¹
JB569 (SEQ ID NO:56)	ITS4 (SEQ ID NO:41)(JB415)	430bp ¹
JB569 (SEQ ID NO:56)	JB572 (SEQ ID NO:59)	346bp ¹
ITS1 (SEQ ID NO:38)(JB410)	JB572 (SEQ ID NO:59)	485bp ¹
JB566 (SEQ ID NO:53)	JB571 (SEQ ID NO:58)	308bp ²
JB569 (SEQ ID NO:56)	JB571 (SEQ ID NO:58)	308bp ²
JB570 (SEQ ID NO:57)	ITS4 (SEQ ID NO:41)(JB415)	501bp ²
JB570 (SEQ ID NO:57)	JB571 (SEQ ID NO:58)	379bp ²
JB570 (SEQ ID NO:57)	JB578 (SEQ ID NO:65)	395bp ²
JB567 (SEQ ID NO:54)	ITS4 (SEQ ID NO:41)(JB415)	450bp ²
JB567 (SEQ ID NO:54)	JB571 (SEQ ID NO:58)	328bp ²
JB567 (SEQ ID NO:54)	JB572 (SEQ ID NO:59)	366bp ²
JB567 (SEQ ID NO:54)	JB578 (SEQ ID NO:65)	344bp ²
JB568 (SEQ ID NO:55)	ITS4 (SEQ ID NO:41)(JB415)	459bp ²
JB568 (SEQ ID NO:55)	JB571 (SEQ ID NO:58)	337bp ²
JB568 (SEQ ID NO:55)	JB572 (SEQ ID NO:59)	375bp ²
JB576 (SEQ ID NO:63)	ITS4 (SEQ ID NO:41)(JB415)	510bp ²
JB576 (SEQ ID NO:63)	JB578 (SEQ ID NO:65)	404bp ²
JB577 (SEQ ID NO:64)	ITS4 (SEQ ID NO:41)(JB415)	495bp ²
JB577 (SEQ ID NO:64)	JB571 (SEQ ID NO:58)	373bp ²
JB577 (SEQ ID NO:64)	JB578 (SEQ ID NO:65)	389bp ²
ITS1 (SEQ ID NO:38)(JB410)	JB571 (SEQ ID NO:58)	447bp ²
ITS1 (SEQ ID NO:38)(JB410)	JB578 (SEQ ID NO:65)	463bp ²
ITS1 (SEQ ID NO:38)(JB410)	JB575 (SEQ ID NO:62)	479bp ²

M. nivale

JB569 (SEQ ID NO:56)	JB575 (SEQ ID NO:62)	340bp
JB567 (SEQ ID NO:54)	JB575 (SEQ ID NO:62)	360bp
JB574 (SEQ ID NO:61)	ITS4 (SEQ ID NO:41)(JB415)	520bp
JB574 (SEQ ID NO:61)	JB572 (SEQ ID NO:59)	436bp

*...Primer combination amplified some fragments by false priming but none were the size of the desired fragment.

5 *....Primers amplified the correct size fragment from both R-type and W-type of *Pseudocercospora herpotrichoides*.

**...Primer combination amplified the correct size fragment from the R-type of *P. herpotrichoides* only.

10 ***....Primer combination amplified the correct size fragment from *F. graminearum*, *F. culmorum*, *F. moniliforme* and *M. nivale*.

****....Primer combination amplified the correct size fragment from *F. graminearum*, *F. culmorum* and *F. moniliforme*.

15

Example 9: Determination of primer specificity to plant tissue infected with fungi

Total genomic DNA was isolated from healthy wheat leaves, wheat leaves infected with *S. nodorum*, wheat leaves infected with *S. tritici* and wheat leaves infected with both *S. nodorum* and *S. tritici* using the protocol described in EXAMPLE 3. PCRs were performed

20 as described in EXAMPLE 4 testing the primer combinations listed in EXAMPLE 8 against DNA from the wheat leaves.

The *S. tritici*-specific primer JB446 (SEQ ID NO:12) and ITS1 (SEQ ID NO:38)(JB410) amplified a 345 bp fragment from purified *S. tritici* DNA, from *S. tritici*-infected wheat leaf tissue and from a wheat leaf sample infected with both *S. tritici* and *S. nodorum*. The primer set did not amplify a diagnostic fragment from healthy wheat leaf tissue nor from *S. nodorum*-infected wheat tissue. Similarly, the *S. tritici*-specific primers JB445 (SEQ ID NO:11) and ITS4 (SEQ ID NO:41)(JB415) amplified a 407 bp fragment from the same tissues as the primer combination JB446 (SEQ ID NO:12) and ITS1 (SEQ ID NO:38)(JB410) and was also diagnostic.

Similarly diagnostic results were obtained with the *S. nodorum*-specific primers JB433 (SEQ ID NO:7) and JB434 (SEQ ID NO:8). The primers amplified a 448 bp fragment from *S. nodorum*-infected wheat tissue, from a wheat leaf sample infested with both *S. nodorum* and *S. tritici*, as well as from purified genomic DNA of *S. nodorum*. The primer combination

JB433 (SEQ ID NO:7) and JB434 (SEQ ID NO:8) did not amplify any fragments from healthy wheat tissue, from *S.tritici*-infected wheat tissue or from purified genomic DNA of *S. tritici*. The *S. nodorum*-specific primers JB527 (SEQ ID NO:10) and JB525 (SEQ ID NO:9) amplified a 458 bp fragment from the same genomic DNAs and wheat tissues as the JB433 (SEQ ID NO:7) and JB434 (SEQ ID NO:8) combination.

The *P. herpotrichoides* primer combinations listed in EXAMPLE 8 were PCR tested against the extracts from wheat stems as obtained in Example 12. PCRs were performed as described in EXAMPLE 4 with the following changes: 35 cycles were run of 94°C for 15 sec 10 and 70°C for 45 sec, 1.5 - 2.5 mM MgCl₂ and 200 μM of each dNTP was used. 1 μl of wheat extract was used in each PCR.

Primer combination JB537 (SEQ ID NO:15) and JB541 (SEQ ID NO:19) amplified a 413 bp fragment from wheat extract infected with the W-type pathotype of *P. herpotrichoides*. No 15 amplification products were produced from amplification with healthy wheat extract nor from wheat extract infected with the R-type pathotype of *P. herpotrichoides*.

The primer combination JB539 (SEQ ID NO:17) and JB544 (SEQ ID NO:22) amplified a 487 bp fragment and primer combination JB540 (SEQ ID NO:18) and JB542 (SEQ ID 20 NO:20) amplified a 413 bp fragment from R-type infected wheat but not from healthy wheat nor from W-type infected wheat.

Total genomic DNA was also isolated from healthy banana leaves and from banana leaves infected with *M. fijiensis* using the protocol described in EXAMPLE 3. PCRs were 25 performed as described in EXAMPLE 4 testing the *M. fijiensis* primer combinations listed in EXAMPLE 8 against DNA from the banana leaves.

The *M. fijiensis*-specific primer JB549 (SEQ ID NO:29) and ITS1 (SEQ ID NO:38)(JB410) amplified a 489 bp fragment from purified *M. fijiensis* DNA and from *M. fijiensis*-infected 30 banana leaf tissue. The primer set did not amplify a diagnostic fragment from healthy banana leaf tissue. The *M. fijiensis*-specific primer combinations JB443 (SEQ ID NO:26)/ITS4 (SEQ ID NO:41)(JB415) and ITS1 (SEQ ID NO:38)(JB410)/JB444 (SEQ ID NO:30) amplified a 418 bp fragment and a 482 bp fragment, respectively, from the same genomic

DNA and banana leaf tissue as the JB549 (SEQ ID NO:29) and ITS1 (SEQ ID NO:38)(JB410) primer combination.

5 **Example 10: Determination of cross-reactivity of species-specific primers with other species and isolates**

Purified fungal genomic DNAs were obtained as described in EXAMPLE 1 and PCR assayed as described in EXAMPLE 4 using the species-specific primers. Other fungal DNA species 10 and isolates were tested for the species-specific primers ability to cross-react with them.

The *S. tritici*-specific primer JB446 (SEQ ID NO:12) and ITS1 (SEQ ID NO:38)(JB410) amplified a 345 bp fragment from all of the *S. tritici* isolates listed in EXAMPLE 1. There was no cross-reactivity with purified genomic DNA of *S. nodorum*, *S. glycines* or *S. 15 passerini*. None of these other fungal species produced an amplification product with the *S. tritici*-specific primers.

A 448 bp fragment was amplified from all of the *S. nodorum* isolates listed in EXAMPLE 1 using the *S. nodorum*-specific primers JB433 (SEQ ID NO:7) and JB434 (SEQ ID NO:8). 20 Similarly the *S. nodorum*-specific primers JB527 (SEQ ID NO:10) and JB525 (SEQ ID NO:9) amplified a 458 bp fragment from all the *S. nosorum* isolates listed in EXAMPLE 1. *S. tritici*, *S. glycines* and *S. passerini* did not produce any amplification products when assayed with the either of the *S. nodorum*-specific primer sets JB433 (SEQ ID NO:7) and JB434 (SEQ ID NO:8) or JB527 (SEQ ID NO:10) and JB525 (SEQ ID NO:9).

25 PCRs were run using the conditions described in EXAMPLE 9, the *P. herpotrichoides*-specific primer combinations listed in EXAMPLE 8 against the other fungal DNA species and isolates listed in EXAMPLE 1.

30 The primer combination JB537 (SEQ ID NO:15) and JB541 (SEQ ID NO:19) produced a 413 bp fragment from the W-type *P. herpotrichoides* isolates only when tested against the *P. herpotrichoides* isolates and the following cereal pathogens: *P. aestiva*, *C. cereale*, *P. sorokiniana*, *S. tritici* and *S. nodorum*. The primer combiantion JB539 (SEQ ID NO:17) and

JB544 (SEQ ID NO:22) amplified a 487 bp fragment from the R-type *P. herpotrichoides* isolate only when tested against the same DNAs. The primer combination JB540 (SEQ ID NO:18) and JB542 (SEQ ID NO:20) produced a 413 bp fragment from the R-type *P. herpotrichoides* isolate only when tested against the same DNAs.

5

Example 11: Sources of Pseudocercospora herpotrichoides-infected wheat

Eyespot-infected wheat stems were received from the stage 1c fungicide screening program of Ciba Basle. Eight day old wheat plants were infected with *P. herpotrichoides* by spraying 10 a conidial suspension (5×10^5 conidia/ml) in 0.2% Tween 20 on the base of the wheat stems. After inoculation, the plants were covered with plastic and incubated for one day at 20°C and 95-100% relative humidity. The plants were transferred to a growth chamber where they were incubated for four weeks at 12°C and 60% relative humidity. After this incubation, the plants were moved to a greenhouse and incubated at 18°C and 60% relative humidity. Wheat 15 plants infected with W-type *P. herpotrichoides* strain 311 were sampled at 8-9 weeks post-infection, while those infected with the R-type strain 308 pathogen were harvested at 9-10 weeks post-infection

Example 12: DNA extraction from wheat stems for *P. herpotrichoides*

20 assay

DNA was extracted from wheat stems using the protocol described by Klimyuk *et al.* (The Plant Journal 3(3):493-494) with some modifications. A 2 cm wheat stem cut 0.5 cm above the basal culm was placed in 160 µl of 0.25 M NaOH and ground with a Kontes pestle until 25 completely macerated. The sample was boiled for 30 s. 160 µl of 0.25 M HCl and 80 µl of 0.5 M Tris-Cl,pH8.0/ 0.25% v/v Nonidet P-40 were added to the sample. The sample was boiled for an additional 2 mins., then placed in an ice water bath. 1 µl of extract was used in the PCR assay.

**Example 13: Incorporation of diagnostic assays into a quantitative
colorimetric assay format**

The colorimetric assay was performed according to Nikiforov *et al.* (PCR Methods and

5 Applications 3:285-291) with the following changes:

1) 30 µl of the R-type PCR product and 3 M NaCl/20 mM EDTA mixture were added to the capture primer well. 50 µl of the W-type PCR product and 3 M NaCl/20 mM EDTA mixture were used in the hybridization reaction.

10

2) The exonuclease treatment and hybridization reaction were incubated at 37°C.

3) A 1:1000 dilution of anti-biotin horseradish peroxidase (HRP) monoclonal antibody was used.

15

4) After a 2 min. incubation with the O-phenylenediamine dihydrochloride (OPD) substrate, 50 µl of 3 N HCl were added to each assay well. 96-well plates were read at 492 nm and referenced at 570 nm using a conventional ELISA plate reader.

20

The primers listed in Table 5 were synthesized as described in EXAMPLE 5 for testing as capture primers for the colorimetric assay.

Table 5: Capture Primer Design for Colormetric Assay

25

Primer

Name Primer Template

Primer Sequence

ITS2 5.8S rDNA

5'GCTGCGTTCTTCATCGATGC3' (SEQ ID NO:39)

30 JB541 W-type *P. herp.*

5'CCACTGATTAGAGGCCGCGAG3'(SEQ ID NO:19)

JB542 R-type *P. herp.*

5'CCACTGATTAGAGGCCGCGAA3'(SEQ ID NO:20)

JB538' W-type *P. herp.*

5'TGACGACTCTAACCCCTACCA3' (SEQ ID NO:66)

JB539' R-type *P. herp.*

5'CGACGACTCTAACCCCTACCG3' (SEQ ID NO:67)

W130 W-type *P. herp.*

5'ATTCAAGGGTGGAGGTCTGA3' (SEQ ID NO:68)

35 R130 R-type *P. herp.*

5'ATTCAAGGGTGGAGGTCTGG3' (SEQ ID NO:69)

JB538'15 W-type *P. herp.*

5'CTCTAACCCCTACCA3' (SEQ ID NO:70)

JB539'15 R-type *P. herp.*

5'CTCTAACCCCTACCG3' (SEQ ID NO:71)

JB553 R & W types

5'GTGGTCCTCTGGCAG3' (SEQ ID NO:72)

JB554 R & W types	5'CTCAACAGCCGAAGC3' (SEQ ID NO:73)
JB555 W-type <i>P. herp.</i>	5'GGGTGGAGGTCTGA3' (SEQ ID NO:74)
JB556 R-type <i>P. herp.</i>	5'GGTGGAGGTCTGG3' (SEQ ID NO:75)
JB561 R-type <i>P. herp.</i>	5'TGGAGGGTCTGGACCA3' (SEQ ID NO:76)
5 JB562 W-type <i>P. herp.</i>	5'TGGAGGGTCTGAACCA3' (SEQ ID NO:77)
JB559 W-type <i>P. herp.</i>	5'AGGGTGGAGGTCTGA3' (SEQ ID NO:78)
JB560 R-type <i>P. herp.</i>	5'AGGGTGGAGGTCTGG3' (SEQ ID NO:79)
JB557 W-type <i>P. herp.</i>	5'TTCTCCGAGAGGCC3' (SEQ ID NO:80)
JB558 R-type <i>P. herp.</i>	5'TTCTCCGAGAGGCC3' (SEQ ID NO:81)

10

The *S. nodorum* diagnostic primers JB527 (SEQ ID NO:10) and JB525 (SEQ ID NO:9) were integrated into the quantitative colormetric assay format. The primer JB527 (SEQ ID NO:10) was synthesized by Midland Certified Reagent Complany (Midland, Texas) to contain a biotin label and the 5' end to contain four internucleotidic phosphorothioate bonds. PCR amplification as described in EXAMPLE 4 using the modified JB527 (SEQ ID NO:10) and JB525 (SEQ ID NO:9) primers from healthy, low, medium, and highly *S. nodorum*-infected wheat produced no, low, medium and high A492 values, respectively, when assayed colometrically using the ITS2 (SEQ ID NO:39) primer as the PCR product capture primer.

15

The *P. herpotrichoides* R-type specific 5' primers, JB539 (SEQ ID NO:17) and JB540 (SEQ ID NO:18), and the *P. herpotrichoides* W-type specific 5' primer, JB537 (SEQ ID NO:15), were also modified to contain a biotin label and four internucleotidic phosphorothioate bonds. A colometric version of the *P. herpotrichoides* R-type PCR assay was developed using the modified JB540 (SEQ ID NO:18) primer, JB542 (SEQ ID NO:20) primer and the capture primer JB539'15. The products produced from amplification from R-type infected wheat and from R-type genomic DNA using the modified JB540 (SEQ ID NO:18) primer and JB542 (SEQ ID NO:20) primer produced positive colometric values when assayed colometrically. Positive colometric values were also obtained by colometric analysis of the PCR products from amplification using the modified JB537 (SEQ ID NO:15) primer and W-type specific primer JB541 (SEQ ID NO:19)with W-type infected wheat and W-type genomic DNA when JB538'15 was used as the capture primer. Furthermore, the intensity of the colometric signal corresponded to the fragment intensity of the PCR product as visualized on an agarose gel.

20

25

30

35

Previously, the different *Septoria* species were identifiable by examination under the microscope, and the identification of the different *Pseudocercospora* strains has been
5 possible only by pathological tests. Similarly, the unambiguous identification of *Mycosphaerella musicola* and *Mycosphaerella fijiensis* has been difficult, and even the isolation of mature perithecia does not always allow accurate identification (Pons, 1990; In:
Sigatoka Leaf Spot Diseases of Banana, Eds. RA Fullerton and RH Stover, International Network for the Improvement of Banana and Plantain, France). Currently immunodiagnostic
10 kits utilizing ELISA technology are routinely used to identify *Septoria tritici*, *Septoria nodorum*, *Pseudocercospora herpotrichoides* and other pathogen, but this technology lacks the accuracy, detection limit and ability to distinguish different isolates of the instant invention. In consequence, the development of a DNA test for the rapid identification of different strains of these fungi offers real advantages not only to fungal taxonomists, but also
15 for disease management and selective fungicide use in the field.

While the present invention has been described with reference to specific embodiments thereof, it will be appreciated that numerous variations, modifications, and further embodiments are possible, and accordingly, all such variations, modifications and
20 embodiments are to be regarded as being within the scope of the present invention.

Deposits

25 The following deposits were made on March 28, 1994, at Agricultural Research Service, Patent Culture Collection (NRRL), Northern Regional Research Center, 1815 North University Street, Peoria, Illinois 61604, U.S.A.:

- | | | |
|----|---|----------------------------|
| 1. | HB101 DH5d (pCRW2-1; SEQ ID NO: 3) | Accession No. NRRL B-21231 |
| 30 | 2. HB101 DH5d (pCRW5-1; SEQ ID. NO: 47) | Accession No. NRRL B-21232 |
| 3. | E. coli DH5d (pCRSTRIT1; SEQ ID NO: 1) | Accession No. NRRL B-21233 |
| 4. | E. coli DH5d (pCRR1-21; SEQ ID NO: 4) | Accession No. NRRL B-21234 |
| 5. | E. coli DH5d (pCRSNOD31; SEQ ID NO: 2) | Accession No. NRRL B-21235 |

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ligon, James M
Beck, James J
- (ii) TITLE OF INVENTION: Detection of Fungal Pathogens Using the Polymerase Chain Reaction
- (iii) NUMBER OF SEQUENCES: 86
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Ciba-Geigy Corporation
 - (B) STREET: 7 Skyline Drive
 - (C) CITY: Hawthorne
 - (D) STATE: NY
 - (E) COUNTRY: USA
 - (F) ZIP: 10532
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US TBA
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/233,608
 - (B) FILING DATE: 04-APR-1994
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Walsh, Andrea C.
 - (B) REGISTRATION NUMBER: 34,988
 - (C) REFERENCE/DOCKET NUMBER: CGC 1739
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 919-541-8666
 - (B) TELEFAX: 919-541-8689

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 548 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..548
 - (D) OTHER INFORMATION: /note= "DNA sequence for the Internal Transcribed Spacer of Septoria tritici"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCCGTAGGTG AACCTGCGGA GGGATCATTA CCGAGCGAGG GCCTCCGGGT CCGACCTCCA	60
ACCCTTTGTG AACACATCCC GTTGCTTCGG GGGCGACCCT GCCGGGCGCC CCCGGAGGAC	120
CACCAAAAAA CACTGCATCT CTGCGTCGGA GTTTACGAGT AAATCGAAAC AAAACTTCA	180
ACAACGGATC TCTTGGTTCT GGCATCGATG AAGAACGCG CGAAATGCGA TAAGTAATGT	240
GAATTGCAGA ATTCACTGAA TCATCGAATC TTTGAACGCA CATTGCGCCC CCTGGTATTG	300
CGGGGGGCAT GCCCGTTCGA GCGTCATTAC ACCACTCCAG CCTCGCTGGG TATGGCGT	360
CTTTTTCGCGG GGGATCACTC CCCCCGCCGC CTCAAAGTCT CCGGCTGAGC GGTCTCGTCT	420
CCCAGCGTTG TGGCATCACG TCTCGCCGCG GAGITCACGA GCCCTCACGG CCGTTAAATC	480
ACACCTCAGG TTGACCTCGG ATCGGGTAGG GATAACCGCT GAACTTAACG ATATCAATAA	540
CGGGAGGA	548

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Septoria nodorum

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..583
- (D) OTHER INFORMATION: /note= "DNA sequence for the Internal Transcribed Spacer of Septoria nodorum"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCCGTAGGTG AACCTGCGGA AGGATCATTA CACTCAGTAG TTTACTACTG TAAAAGGGC	60
TGTTAGTCTG TATAGCGCAA GCTGATGAGC AGCTGGCCTC TTTTATCCAC CCTTGCTTT	120
TGCGTACCCA CGTTCCCTCG GCAGGCTTGC CTGCCGGTTG GACAAATTAA TAACCTTTT	180
AATTTCAAT CAGCGTCTGA AAAACTTAAT AATTACAACG TTCAACAAACG GATCTCTTGG	240
TTCTGGCATC GATGAAGAAC GCAGCGAAAT GCGATAAGTA GTGTGAATTG CAGAATTCA	300
TGAATCATCG AATCTTGAA CGCACATTGC GCCCCCTGGT ATTCCATGGG GCATGCCGT	360
TCGAGCGTCA TTGTACCCCT CAAGCTCTGC TTGGTGTGAG GTGTTTGTCC TCTCCCTAGT	420
GTTTGGACTC GCCTTAAAT AATTGGCAGC CAGTGTGTTG GTATTGAAGC GCAGCACAAG	480
TCGGGATTCTG TAACAAACAC TTGGTCCAC AAGCCTTTTAACTTTGAC CTGGATCAG	540
GTACGGATAAC CCGCTGAAC TAAGCATATC AATAAGCGGA GGA	583

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 626 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Pseudocercosporaella herpotrichoides
 - (B) STRAIN: Strain R
 - (C) INDIVIDUAL ISOLATE: Variant W2-1
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..626
 - (D) OTHER INFORMATION: /note= "DNA sequence for the Internal Transcribed Spacer of Pseudocercosporaella herpotrichoides strain W (variant W2-1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCCGTAGGTG AACCTGCGGA AGGATCATTA ATAGAGCAAT GAACAGACAG CGCCCCGGGA	60
GAAATCCTGG GGGCTACCCCT ACTTGGTAGG GTTTAGAGTC GTCAGGCCGC TCGGAGAACG	120
CTGGTTCAAGA CCTCCACCCCT TGAATAAAATT ACCTTTGTTG CTTTGGCAGG GCGCCTCGCG	180
CCAGCGGCTT CGGCTGTTGA GTACCTGCCA GAGGACCACA ACTCTTGTCT TTAGTGATGT	240
CTGAGTACTA TATAATAGTT AAAACTTTCA ACAACGGATC TCTTGGTTCT GGCATCGATG	300
AAGAACGCAG CGAAATGCGA TAAGTAATGT GAATTGCAGA ATTCAAGTGAA TCATCGAATC	360
TTTGAACGCA CATTGCGCCC TCTGGTATTTC CGGGGGGCAT GCCTGTTCGA GCGTCATTAT	420
AACCACTCAA GCTCTCGCTT GGTATTGGGG TTCGCGTCCT CGCGGCCTCT AAAATCAGTG	480
GCGGTGCCTG TCGGCTCTAC GCGTAGTAAT ACTCCTCGCG ATTGAGTCCG GTAGGTTAC	540
TTGCCAGTAA CCCCAATT TTTACAGGTT GACCTCGGAT CAGGTAGGGA TACCCGCTGA	600
ACTTAAGCAT ATCAATAAGC GGAGGA	626

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 627 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Pseudocercosporaella herpotrichoides
 - (B) STRAIN: Strain R

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..627
- (D) OTHER INFORMATION: /note= "DNA sequence for the Internal Transcribed Spacer of Pseudocercosporaella herpotrichoides Strain R"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCCGTAGGTG AACCTGCGGA AGGATCATTA ATAGAGCAAT GGATAGACAG CGCCCCGGGA	60
GAAATCCTGG GGGCCACCCCT ACTTCGGTAA GGTTTAGAGT CGTCGGGCCT CTCGGAGAAC	120
CCTGGTCCAG ACCTCCACCC TTGAATAAAT TACCTTGTT GCTTTGGCAG GGCGCCTCGC	180
GCCAGCGGCT TCGGCTGTT AGTACCTGCC AGAGGACCAC AACTCTTGTT TTTAGTGATG	240
TCTGAGTACT ATATAATAGT TAAAACTTTC ACAACGGAT CTCTTGGTTC TGGCATCGAT	300
GAAGAACGCA GCGAAATGCG ATAAGTAATG TGAATTGCAG AATTCACTGAA ATCATCGAAT	360
CTTTGAACGC ACATTGCGCC CTCTGGTATT CGGGGGGCA TGCCCTGTTCC AGCGTCATTA	420
TAACCACTCA AGCTCTCGCT TGGTATTGGG GTTCGCGTCT TCGCGGCCCTC TAAAATCAGT	480
GGCGGTGCCT GTCGGCTCTA CGCGTAGTAA TACTCCTCGC GATTGAGTCC GGTAGGTTA	540
CTTGCCAGCA ACCCCCAATT TTTTACAGGT TGACCTCGGA TCAGGTAGGG ATACCCGCTG	600
AACTTAAGCA TATCAATAAG CGGAGGA	627

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycosphaerella fijiensis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..534
- (D) OTHER INFORMATION: /note= "DNA sequence for the Internal Transcribed Spacer of Mycosphaerella fijiensis"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCCGTAGGTG AACCTGCGGA GGGATCATTA CCGAGTGAGG GCTCACGCC GACCTCCAAC	60
CCTTTGTGAA CCACAACCTTG TTGCTTCGGG GGCGACCTGC CGTCGGCGGG CGCCCCCGGA	120
GGCGGTCTAA ACACTGCATC TTTGCGTCGG AGTTTAAAC AAATCGAACAA AAACTTCAA	180
CAACGGATCT CTTGGTTCTG GCATCGATGA AGAACGCAGC GAAATGCGAT AAGTAATGTG	240
AATTGCAGAA TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCT TTGGTATTCC	300

GAAGGGCATG CCTGTTCGAG CGTCATTCA CCACTCAAGC CTGGCTTGGT ATTGGGCCTC	360
GCGGTTCTTC GCGGCCCTTA AAGTCTCCGG CTGAGCTGTC CGTCTCTAAG CGTTGTGGAT	420
CTTTCAATTG GCTTCGGAGT GCGGGTGGCC GCGGCCGTTA AATCTTTATT CAAAGGTTGA	480
CCTCGGATCA GGTAGGGATA CCCGCTGAAC TTAAGCATAT CAATAAGCGG AGGA	534

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycosphaerella musicola

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..540
 - (D) OTHER INFORMATION: /note= "DNA sequence for the Internal Transcribed Spacer of Mycosphaerella musicola"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCCGTAGGTG AACCTGCGGG GGGATCATTA CCGAGTGAGG GCTCACCCCC GACCTCCAAC	60
CCTTTGTGAA CCACACCTGT TGCTTCGGGG GCGACCCTGC CGCGAACCTT GTGCCGGGC	120
GCCCCCGGAG GTCTCCTTAA CACTGCATCT CTGCGTCGGA GTTCAAACA AATCGGACAA	180
AACTTTCAAC AACGGATCTC TTGGTTCTGG CATCGATGAA GAACGCAGCG AAATGCGATA	240
AGTAATGTGA ATTGCAGAAT TCAGTGAATC ATCGAATCTT TGAACGCACA TTGCGCCCTT	300
TGGCATTCCG AAGGGCATGC CTGTTCGAGC GTCATTTCAC CACTCAAGCC TAGCTTGGTA	360
TTGGGGCCCG CGGTGCTCCG CGCGCCCCAA AGTCTCCGG CTAAGCCGTC CGTCCTAAG	420
CGTTGTGGAT TTTTCAGTTC GCTCCGGAGC GCGGGTGGCC GCGGCCGTTA AATCTTCAAA	480
GGTTGACCTC GGATCAGGTA GGGATACCCG CTGAACCTAA GCATATCAAT AACCGGAGGA	540

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Other nucleic acid
 - (A) DESCRIPTION: Oligonucleotide primer JB433

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACACTCAGTA GTTTACTACT

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Oligonucleotide primer JB434

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGTGCTGC GC TTCAATA

17

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Oligonucleotide primer JB525

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGACTTGIG CTGGCCTTCA ATA

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Oligonucleotide primer JB527

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CATTACACTC AGTAGTTTAC TACT

24

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
 (A) DESCRIPTION: Oligonucleotide primer JB445

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTGCGTCGGGA GTTTACG

17

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
 (A) DESCRIPTION: Oligonucleotide primer JB446

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAGGGCTGGA GTGGTGT

17

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
 (A) DESCRIPTION: Oligonucleotide primer JB526

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCCAGCGAGG CTGGAGTGTT GT

22

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid
 - (A) DESCRIPTION: Oligonucleotide primer JB536
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTGGGGGCTA CCCTACTTGG TAG

23

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid
 - (A) DESCRIPTION: Oligonucleotide primer JB537
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGGGGCTACC CTACTTGGTA G

21

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid
 - (A) DESCRIPTION: Oligonucleotide primer JB538
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACTTGGTAGG GTTTAGAGTC GTCA

24

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: Oligonucleotide primer JB539

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTTCGGTAAG GTTTAGAGTC GTCG

24

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: Oligonucleotide primer JB540

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGGGGCCACC CTACTTCGGT AA

22

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: Oligonucleotide primer JB541

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCACTGATTT TAGAGGCCGC GAG

23

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: Oligonucleotide primer JB542

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCACTGATT TAGAGGCCGC GAA

23

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Oligonucleotide primer JB543

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCTGTAAAAAA ATTGGGGGTT A

21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Oligonucleotide primer JB544

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCTGTAAAAAA ATTGGGGGTT G

21

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Oligonucleotide primer JB547

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATTACCGAGT GAGGGCTCAC GC

22

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Oligonucleotide primer JB548

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTTGCTTCGG GGGCGACCTG

20

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Oligonucleotide primer JB442

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCGGGGGCCGA CCTGCCG

17

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Oligonucleotide primer JB443

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCGGAGGCCG TCTA

14

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: Oligonucleotide primer JB545

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCACAACGCT TAGAGACGGA CAG

23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: Oligonucleotide primer JB546

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CACCCGCACT CCGAACGAA TT

22

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: Oligonucleotide primer JB549

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCCGAGGT CAACCTTTGA ATAA

24

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
 (A) DESCRIPTION: Oligonucleotide primer JB444

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGTCAACCTT TGAATAA

17

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
 (A) DESCRIPTION: Oligonucleotide primer JB451

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCTTTGTGAA CCACACCT

18

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
 (A) DESCRIPTION: Oligonucleotide primer JB440

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTGCCGGCGA ACTT

14

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: Oligonucleotide primer JB449

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ACCCCTGCCGG CGAACTT

17

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: Oligonucleotide primer JB448

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCGACCCTGC CGGCGAAC

18

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: Oligonucleotide primer JB441

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TAGCCGGGAG ACTTTG

17

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: Oligonucleotide primer JB450

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TCTGCGTCGG AGTTCC

16

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Oligonucleotide primer JB452

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CCCGCGCTCCG GAGCGAAC

18

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Oligonucleotide primer ITS1

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCCGTAGGTG AACCTGCGG

19

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Oligonucleotide primer ITS2

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GCTGCGTCTC TCATCGATGC

20

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Oligonucleotide primer ITS3

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCATCGATGA AGAACGCAGC

20

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Oligonucleotide primer ITS4

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCCTCCGCTT ATTGATATGC

20

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Oligonucleotide primer OPB-12

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCTTGACCCA

10

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Oligonucleotide primer OPE-6

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AAGACCCCTC

10

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Oligonucleotide primer OPE-12

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTATCGCCCC

10

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Oligonucleotide primer OPE-19

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACCCCCGAAG

10

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Oligonucleotide primer OPE-15

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACGCACAAACC

10

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Pseudocercosporrella herpotrichoides
- (B) STRAIN: Strain W
- (C) INDIVIDUAL ISOLATE: Variant W5-1

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..627
- (D) OTHER INFORMATION: /note= "DNA sequence for the Internal Transcribed Spacer of Pseudocercosporrella herpotrichoides strain W (variant W5-1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TCCGTAGGTG AACCTGCGGA AGGATCATTA ATAGAGCAAT GAACAGACAG CGCCCTGGGA	60
GAAATCCTGG GGGCTACCCCT ACTTCGGTAG GGTTTAGAGT CGTCAGGCCT CTCGGAGAAC	120
CCTGGTTCAAG ACCTCCACCC TTGAATAAAT TACCTTGTT GCTTTGGCAG GGCGCCTCGC	180
GCCAGCGGCT TCGGCTGTTG AGTACCTGCC AGAGGACCAC AACTCTGTT TTTAGTGATG	240
TCTGAGTACT ATATAATAGT TAAAACTTTC AACAAACGGAT CTCTTGGTTC TGGCATCGAT	300
GAAGAACGCA GCGAAATGCG ATAAGTAATG TGAATTGCAG AATTCAAGTGA ATCATCGAAT	360
CTTTGAACGC ACATTGCGCC CTCTGGTATT CCGGGGGGCA TGCGCTGTTCG AGCGTCATTA	420
TAACCACTCA AGCTCTCGCT TGGTATTGGG GTTCGCGTCC TCGCGGCCTC TAAAATCAGT	480

GGCGGTGCCT CTCGGCTCTA CGCGTAGTAA TACTCCTCGC GATTGAGTCC GGTAGGTTA	540
CTTGCCAGTA ACCCCAATT TTTTACAGGT TGACCTCGGA TCAGGTAGGG ATACCCGCTG	600
AACTTAAGCA TATCAAATAAG CGGAGGA	627

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
 (A) DESCRIPTION: M13 universal -20 oligonucleotide primer

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GTAAAACGAC GGCCAGT 17

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid
 (A) DESCRIPTION: M13 universal reverse oligonucleotide primer

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AACAGCTATG ACCATG 16

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide primer
 JB563"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CTTGCCTGCC GGTGGACAA ATT

23

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide JB564"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTCAGTAGTT TACTACTGTA AAAGG

25

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide JB565"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTTCTGGACG CAAGTGTTTG TTAC

24

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide JB566"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GTTTTTAGTG GAACTTCTGA GT

22

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide JB567"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CGCAGGAACC CTAACCTCT

19

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide primer JB568"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GCCCCGGCGCA GG

12

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide primer JB569"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

RTWWTTWRTG GAMYYTCTGA GT

22

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide primer JB570"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TATGTTGCCT CGGGCG

16

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer
JB571"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TAACGATATG TAAATTACTA CGCT

24

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer
JB572"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AAGTTGGGT TTAACGGC

18

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer JB
573"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

AGCGAGCCCCG CCAC

14

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer
JB574"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCATTGTGAA CGTTACCTAT AC

22

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer
JB575"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGACCAGAGC GAGATGTA

18

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer
JB576"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTGAACATAC CTTATGTTGC C

21

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide primer

JB577*

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTTGCCTCGG CGGATC

16

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide primer

JB578*

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CCGCGACCAT TACCA

16

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide primer

JB538**

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TGACGACTCT AAACCCTACC A

21

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

49

(A) DESCRIPTION: /desc = "Oligonucleotide primer
JB539"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CGACGACTCT AACACCTTACC G

21

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer
W130"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ATTCAAGGGT GGAGGTCTGA

20

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer
R130"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATTCAAGGGT GGAGGTCTGG

20

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer
JB539'15"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CTCTAAACCC TACCA

15

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer
JB539 '15"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CTCTAACCT TACCG

15

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer
JB553"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GTGGTCCTCT GGCAG

15

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer
JB554"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CTCAACAGCC GAAGC

15

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide primer
 JB555"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GGGTGGAGGT CTGA

14

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide primer
 JB556"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GGTGGAGGTC TGG

13

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide primer
 JB561"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TGGAGGTCTG GACCA

15

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer
JB562"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TGGAGGTCTG AACCA

15

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer
JB559"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

AGGGTGGAGG TCTGA

15

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer
JB560"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGGGTGGAGG TCTGG

15

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer
JB557"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TTCTCCGAGA GGCGT

15

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer
JB558"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTCTCCGAGA GGCGCC

15

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..504
- (D) OTHER INFORMATION: /note= "DNA sequence for the internal transcribed spacer region of Fusarium culmorum (fculg.con)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAGGGATCAT TACCGAGTTT ACTRACTCCC AAACCCCTGT GAACDTACCT TATGTTGCCT	60
CGGCGGATCA GCCCGCGCCC CGTAAAAAGG GACGGCCCGC CGCAGGAACC CTAAACTCTG	120
TTTTTAGTGG AACTTCTGAG TATAAAAAC AAATAATCA AAACTTCAA CAACGGATCT	180
CTTGGTCTG GCATCGATGA AGAACGCAGC [AAAATGCGAT AAGTAATGTG AATTGCAGAA	240
TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGGCCCG CCAGTATTCT GGCGGGCATG	300
CCTGTTGAG CGTCAT[]TCA ACCCTCAAGC CCAGCTTGGT GTTGGGAGCT GCAGTCCTGC	360
TGCACCCCCC AAATACATTG GCGGTCACGT CGRAGCTTCC ATAGCGTAGT AATTACATA	420
TCGTTACTGG TAATCGTCGC GGCGYACGCCG TTAAAC[]CCA ACT[]CTGAAT GTTGACCTCG	480

Seq. 6
2-108

54 Seq. 59

GATCAGGTAG GAATACCCGC TGAA

504

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..503

(D) OTHER INFORMATION: /note= "DNA sequence for the internal transcribed spacer region of Fusarium graminearum (fgram.con)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GGATCATTAC CGAGTTTACW SACTCCAAA CCCCTGTGAA CATACTTAT GTTGCCTCGG	60
CGGATCAGCC CGCGCCCCGA AAGGGACGGC CCGCCGCAGG AACCTAAAC TCTGTTTTA	120
GTGGAACCTTC TGAGTATAAA AAACAAATAA ATCAAAACTT TCAACAACGG ATCTCTTGGT	180
KCTGGCATCG ATGAAGAACG CASCRAAATG CGATAAGTAA TGTGWATTGC AGAATTCACT	240
GAATCAWCAGA ATCTTTGAAC GCWSATTGCK MCCRCCAGTA TTCTGGCGGG CATGCCGTGTT	300
CGAGCGTCAT TTCAACCCTC AAGCCCAGVT TGGTGTKGGG GARYTGCAGK CCTTRYTKCAC	360
TCCCCAAATA ARTTGGCGGT CACGTCGAAC TTCCATAGCG TAGTAAGTTA CACATCGTTA	420
CTGGTAATCG TCGCGGCTAC GCCGTTAAC [CCCAACTTCT GAATGTTGAC] CTCGGATCAG	480
GTAGGAATAC CCGCTGAAGG TAA	503

Seq. 59

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..353

(D) OTHER INFORMATION: /note= "DNA sequence for the internal transcribed spacer region of Fusarium moniliforme (fmono.con)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TCCGTAGGTG AACCTGCGGA TAGGRGTCAT TASMGAGTTT ACWACTSCCA AACCCCTGTG	60
AAYATACCTT ATGTTGCSTC GGCGGATCAG CCCGCGCSCC GTARRAAGGG ACGGCCCGCC	120

55

GCAGGAACCC TAAACTCTGT TTTTAGTGG AACTCTGAGT ATAAAAAACA AATAAATCAA	180
AACTTTCAAC AACGGATCTC TTGGTTCTGG CATCGATGAA GAACGCAGCA AAATGCGATA	240
AGTAATGTGA ATTGCAGAAT TCAGTGAATC ATCGAATCTT TGAACGCACA TTGYGMCCGC	300
CAGTATTCTG GCGGGCATGC CTGTTGAGC GTCATTCAA CCCTCAAGCC CAG	353

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 545 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..545
- (D) OTHER INFORMATION: /note= "DNA sequence for the internal transcribed spacer region of Microdochium nivale (mnivale.txt)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GCGGATCATT ACAGAGTTGC AAAACTCCCT AAACCATTGT GAACGTTACC TATAACCGTTG	60
CTTCGGCGGG CGGCCCGGG GTTTACCCCC CGGRAGYCCC TGGKMKCCCAC CGCGGGSGCC	120
MGCCGGAGGT CACCAAACTC TTGATAATTT ATGGCCTCTC TGAGTCTTCT GTACTGAATA	180
AGTCAAAACT TTCAACAAACG GATCTCTTGG TTCTGGCATC GATGAAGAAC GCAGCGAAAT	240
GCGATAAGTA ATGTGAATTG CAGAATTCAAG TGAATCATCG AATCTTGAA CGCACATTGC	300
GCCCCGCCAGC ATTCTGGCGG GCATGCCGTG TCGAGCGTCA TTTCAACCAT CAAGCCCCG	360
GGCTTGTGTT GGGGACCTRGC GGCTGCCGCA GGCCCTGAAA AGCAGTGTGCG GGCTCGCTGT	420
CGCACCGAGM GTAGTAGSAT ACATCTCGCT CTGGTCGCGC CGCGGGTTCC GGCCGTTAAA	480
CCACCTTTT AACCCAAGGT TGACCTCGGA TCAGGTAGGA AGACCCGCTG AACTTACGCA	540
TATCA	545

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 563 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..563
- (D) OTHER INFORMATION: /note= "DNA sequence for the

internal transcribed spacer of Septoria avenae f. sp. tricicea
ATCC# 26380 (satits.con)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TCCCCGTAGGT GAACCTGCGG AAGGATCATT ACACTCAGTA GTTTACTACT GTAAAGGAGG	60
CTGTTAGTCT GTATAGCGCA AGCTGATGAG CAGCTAGCCT CTTTTATCCA CCCTTGCTT	120
TTGCGTACCC ACGTTTCCTC GGCAGGCTTG CCTGCCGATT GGACAAACCT ATAACCTTTT	180
TAATTTCAA TCAGCGTCTG AAAAACCTAA TAATTACAAC TTTCAACAAAC GGATCTCTTG	240
GTTCTGGCAT CGATGAAGAA CGCAGCGAAA TGCGATAAGT AGTGTGAATT GCAGAATTCA	300
GTGAATCATC GAATCTTGA ACGCACATTG CGCCCCTTGG TATTCCATGG GGCATGCCCTG	360
TTCGAGCGTC ATTTGTACCC TCAAGCTCTG CTTGGTGTG GGTGTTGTC CTCTCCCTAG	420
TGTTTGGACT CGCCTTAAAA TAATTGGCAG CCAGTGTGTTT GGTAYTGAAG CGCAGCACAA	480
GTCGCGATTC TTATCAAATA CTTGCGTCCA CAAGCCCTTT TTTAACTTTT GACCTCGGAT	540
CAGGTAGGAG ACCGCTGACT TAA	563

What is claimed is:

1. A DNA sequence encoding an Intervening Transcribed Sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 47, SEQ ID NO: 82, SEQ ID NO: 83, and SEQ ID NO: 84, SEQ ID NO: 85, and SEQ ID NO: 86.
2. An oligonucleotide primer for use in amplification-based detection of a fungal Intervening Transcribed Sequence wherein said primer is derived from the DNA sequence of claim 1.
3. The oligonucleotide of claim 2, wherein said primer is selected from the group consisting of SEQ ID NOS: 7 to 37 and SEQ ID NOS: 50 to 65.
4. A pair of oligonucleotide primers for use in the amplification-based detection of a fungal Intervening Transcribed Sequence, wherein at least one primer is selected from the group consisting of SEQ ID NOS: 7 to 37 and SEQ ID NOS: 50 to 65.
5. The pair of oligonucleotide primers according to claim 4, wherein one primer is selected from the group consisting of SEQ ID NOS: 7 to 37 and SEQ ID NOS: 50 to 65 and the other primer is selected from the group consisting of SEQ ID NOS: 38 to 41.
6. The pair of oligonucleotide primers according to claim 4, wherein said pair is selected from the group consisting of pairs of Table 4.
7. The pair of oligonucleotide primers according to claim 4 wherein said pair is selected from the group consisting SEQ ID NO: 7 and SEQ ID NO: 8.
8. The pair of oligonucleotide primers according to claim 5, wherein said pair is selected from the group consisting of
 - (a) SEQ ID NO: 10 and SEQ ID NO: 9;
 - (b) SEQ ID NO: 12 and SEQ ID NO: 38;

- (c) SEQ ID NO: 11 and SEQ ID NO: 41;
- (d) SEQ ID NO: 29 and SEQ ID NO: 38;
- (e) SEQ ID NO: 7 and SEQ ID NO: 41;
- (f) SEQ ID NO: 30 and SEQ ID NO: 38;
- 5 (g) SEQ ID NO: 15 and SEQ ID NO: 19;
- (h) SEQ ID NO: 17 and SEQ ID NO: 22;
- (i) SEQ ID NO: 18 and SEQ ID NO: 20; and
- (j) SEQ ID NO: 26 and SEQ ID NO: 41.

10 9. An oligonucleotide primer for identification of a fungal pathogen, wherein said primer is selected from the group of primers consisting of SEQ ID NO: 42 to 46.

10. A method for the detection of a fungal pathogen, comprising the steps of:

(a) isolating DNA from a plant leaf infected with a pathogen;

15 (b) amplifying a part of the intervening transcribed region of said pathogen using said DNA as a template in a polymerase chain reaction with a pair of primers according to claims 4 or 5; and

(c) visualizing said amplified part of the intervening transcribed region.

20 11. The method of claim 10, wherein said fungal pathogen is selected from *S. nodorum*, *S. tritici*, *P. herpotrichoides*, *M. fijiensis*, *M. musicola*, *F. culmorum*, *F. graminearum*, *Microdochium nivale*, and *F. moniliforme*.

25 12. The method of claim 10, wherein said *P. herpotrichoides* is selected from strain W and strain R.

13. A method for the detection of a fungal pathogen, comprising the steps of:

(a) isolating DNA from a plant leaf infected with a pathogen;

30 (b) subjecting said DNA to polymerase chain reaction amplification using at least one primer according to claim 9; and

(c) visualizing the product or products of said polymerase chain reaction amplification.

14. A kit comprising a carrier being compartmentalized to receive in close confinement therein one or more container means, one of said container means containing the primer of claim 2.

5 15. A kit comprising a carrier being compartmentalized to receive in close confinement therein one or more container means, one of said container means containing the primer of claim 3.

10 16. A kit comprising a carrier being compartmentalized to receive in close confinement therein one or more container means, one of said container means containing the primers of claim 4.

15 17. A kit comprising a carrier being compartmentalized to receive in close confinement therein one or more container means, one of said container means containing the primer of claim 5.

18. A kit comprising a carrier being compartmentalized to receive in close confinement therein one or more container means, one of said container means containing the primer of claim 13.

20 19. In a quantitative colorimetric assay for the detection of a fungal pathogen comprising the steps of (a) isolating DNA from a plant leaf infected with a pathogen; (b) amplifying the DNA region of said pathogen in a polymerase chain reaction; and (c) visualizing said amplified part of the intervening transcribed region

25 wherein said improvement comprises amplifying said DNA from a part of the intervening transcribed region of said pathogen using as a template a pair of primers according to claims 4 as the diagnostic primers and visualizing said amplified part using a capture primer wherein said capture primer is selected from the group consisting of a primer of Table 5.

30 20. The assay of claim 19 wherein said diagnostic primers are selected from SEQ ID NO.: 10 and SEQ ID NO.: 9 and the capture primer is SEQ ID NO.: 39.

21. The assay of claim 19 wherein said diagnostic primers are selected from SEQ ID NO.: 18 and SEQ ID NO.: 20 and the capture primer is SEQ ID NO.: 71.

22. The assay of claim 19 wherein said diagnostic primers are selected from SEQ ID

5 NO.: 15 and SEQ ID NO.: 19 and the capture primer is SEQ ID NO.: 71.

FIGURE 1

FIGURE 2

FIGURE 3